

RAW SEQUENCE LISTING

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Application Serial Number: 10/526,940
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DATE: 02/27/2006

PATENT APPLICATION: US/10/526,940

TIME: 14:38:35

Input Set : A:\BB-137.ST25.txt

Output Set: N:\CRF4\02272006\J526940.raw

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3 <110> APPLICANT: Deuschle, Ulrich
4      Heck, Stefanie
5      Kober, Ingo
6      Bauer, Ulrike
7      Balogh, Imola
9 <120> TITLE OF INVENTION: NR3B1 Nuclear Receptor Binding 3-Substituted Pyrazoles
11 <130> FILE REFERENCE: BB-137
13 <140> CURRENT APPLICATION NUMBER: 10/526,940
14 <141> CURRENT FILING DATE: 2005-03-08
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/007066
17 <151> PRIOR FILING DATE: 2003-07-02
19 <150> PRIOR APPLICATION NUMBER: EP 02020256.0
20 <151> PRIOR FILING DATE: 2002-09-10
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: PatentIn version 3.3
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27 <211> LENGTH: 1377
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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36 acggaacctt ccagcccagc ctccctgacg gacagcgtca accaccacag ccctgggtggc      180
38 tcttcagacg ccagtgggag ctacagtcca accatgaatg gccatcagaa cggacttgac      240
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42 tatgatgact gctccagcac cattgttgaa gatccccaga ccaagtgtga atacatgctc      360
44 aactcgaatg ccaagagact gtgttttagt tgtggtgaca tcgcttctgg gtaccactat      420
46 ggggtagcat catgtgaagc ctgcaaggca ttcttcaaga ggacaattca aggcaatata      480
48 gaatacagct gccctgccac gaatgaatgt gaaatcacia agcgcagacg taaatcctgc      540
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54 tacctgaacc ctgagctggt tcagccagcc aaaaagccat ataacaagat tgtctcacat      720
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66 ggccttcttg atctaaataa tgctatcctg cagctggtaa agaaatacaa gagcatgaag      1080
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89 agcagccggc gggcgccgcc gagtgagggg acgcggcgcg gtggggcggc gcggcccagag      180
91 gaggcggcgg aggagggggc gcccgcggcc ccggtctcac tccggcactc cgggcccgtc      240
93 ggcccccatg cctgcccagc cgcgctgccg gagccccagg tgaccagcgc catgtccagc      300
95 caggtggtgg gcattgagcc tctctacatc aaggcagagc cggccagccc tgacagtcca      360
97 aagggttcct cggagacaga gaccgagcct cctgtggccc tggcccctgg tccagctccc      420
99 actcgctgcc tcccaggcca caaggaagag gaggatgggg agggggctgg gcctggcgag      480
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103 gacgtggcct ccggtacca ctatggtgtg gcctcctgtg aggcctgcaa agccttcttc      600
105 aagaggacca tccaagggag catcgagtac agctgtcccg cctccaacga gtgtgagatc      660
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129 gatgagccga ggctgtggag cagctgcgag aagctcctgc acgaggccct gctggagtat      1380
131 gaagccggcc gggctggccc cggagggggg gctgagcggc ggccggcggg caggctgctg      1440
133 ctcacgctac cgctcctccg ccagacagcg ggcaaagtgc tggcccattt ctatgggggtg      1500
135 aagctggagg gcaaggtgcc catgcacaag ctgttcttgg agatgctcga ggccatgatg      1566
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141 <211> LENGTH: 25
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145 <400> SEQUENCE: 3
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151 Arg Leu Leu Gln Glu Gly Ser Pro Ser
152          20          25
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156 <211> LENGTH: 29
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 4
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164 <210> SEQ ID NO: 5
165 <211> LENGTH: 29

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167 <213> ORGANISM: Homo sapiens
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175 <212> TYPE: PRT
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184 Lys Thr Glu Pro Ser Ser Pro Ser Ser Gly Ile Asp Ala Leu Ser His
185 20 25 30
188 His Ser Pro Ser Gly Ser Ser Asp Ala Ser Gly Gly Phe Gly Leu Ala
189 35 40 45
192 Leu Gly Thr His Ala Asn Gly Leu Asp Ser Pro Pro Met Phe Ala Gly
193 50 55 60
196 Ala Gly Leu Gly Gly Thr Pro Cys Arg Lys Ser Tyr Glu Asp Cys Ala
197 65 70 75 80
200 Ser Gly Ile Met Glu Asp Ser Ala Ile Lys Cys Glu Tyr Met Leu Asn
201 85 90 95
204 Ala Ile Pro Lys Arg Leu Cys Leu Val Cys Gly Asp Ile Ala Ser Gly
205 100 105 110
208 Tyr His Tyr Gly Val Ala Ser Cys Glu Ala Cys Lys Ala Phe Phe Lys
209 115 120 125
212 Arg Thr Ile Gln Gly Asn Ile Glu Tyr Ser Cys Pro Ala Thr Asn Glu
213 130 135 140
216 Cys Glu Ile Thr Lys Arg Arg Arg Lys Ser Cys Gln Ala Cys Arg Phe
217 145 150 155 160
220 Met Lys Cys Leu Lys Val Gly Met Leu Lys Glu Gly Val Arg Leu Asp
221 165 170 175
224 Arg Val Arg Gly Gly Arg Gln Lys Tyr Lys Arg Arg Leu Asp Ser Glu
225 180 185 190
228 Ser Ser Pro Tyr Leu Ser Leu Gln Ile Ser Pro Pro Ala Lys Lys Pro
229 195 200 205
232 Leu Thr Lys Ile Val Ser Tyr Leu Leu Val Ala Glu Pro Asp Lys Leu
233 210 215 220
236 Tyr Ala Met Pro Pro Pro Gly Met Pro Glu Gly Asp Ile Lys Ala Leu
237 225 230 235 240
240 Thr Thr Leu Cys Asp Leu Ala Asp Arg Glu Leu Val Val Ile Ile Gly
241 245 250 255
244 Trp Ala Lys His Ile Pro Gly Phe Ser Ser Leu Ser Leu Gly Asp Gln
245 260 265 270
248 Met Ser Leu Leu Gln Ser Ala Trp Met Glu Ile Leu Ile Leu Gly Ile
249 275 280 285
252 Val Tyr Arg Ser Leu Pro Tyr Asp Asp Lys Leu Val Tyr Ala Glu Asp
253 290 295 300
256 Tyr Ile Met Asp Glu Glu His Ser Arg Leu Ala Gly Leu Leu Glu Leu
257 305 310 315 320

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260 Tyr Arg Ala Ile Leu Gln Leu Val Arg Arg Tyr Lys Lys Leu Lys Val
261          325          330          335
264 Glu Lys Glu Glu Phe Val Thr Leu Lys Ala Leu Ala Leu Ala Asn Ser
265          340          345          350
268 Asp Ser Met Tyr Ile Glu Asp Leu Glu Ala Val Gln Lys Leu Gln Asp
269          355          360          365
272 Leu Leu His Glu Ala Leu Gln Asp Tyr Glu Leu Ser Gln Arg His Glu
273          370          375          380
276 Glu Pro Trp Arg Thr Gly Lys Leu Leu Leu Thr Leu Pro Leu Leu Arg
277 385          390          395          400
280 Gln Thr Ala Ala Lys Ala Val Gln His Phe Tyr Ser Val Lys Leu Gln
281          405          410          415
284 Gly Lys Val Pro Met His Lys Leu Phe Leu Glu Met Leu Glu Ala Lys
285          420          425          430
288 Ala Trp Ala Arg Ala Asp Ser Leu Gln Glu Trp Arg Pro Leu Glu Gln
289          435          440          445
292 Val Pro Ser Pro Leu His Arg Ala Thr Lys Arg Gln His Val His Phe
293          450          455          460
296 Leu Thr Pro Leu Pro Pro Pro Pro Ser Val Ala Trp Val Gly Thr Ala
297 465          470          475          480
300 Gln Ala Gly Tyr His Leu Glu Val Phe Leu Pro Gln Arg Ala Gly Trp
301          485          490          495
304 Pro Arg Ala Ala
305          500
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309 <211> LENGTH: 1503
310 <212> TYPE: DNA
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318 gccagcggcg gctttggcct ggccctgggc acccagccca acggtctgga ctgcgaaccc      180
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322 agcggcatca tggaggactc ggccatcaag tgcgagtaca tgctcaacgc catccccaag      300
324 cgctgtgtcc tcgtgtgcgg ggacattgcc tctggctacc actacggcgt ggcctcctgc      360
326 gaggcttgca aggcccttct caagaggact atccaaggga acattgagta cagctgcccg      420
328 gccaccaacg agtgcgagat caccaaacgg aggcgcaagt cctgccaggc ctgccgcttc      480
330 atgaaatgcc tcaaagtggg gatgctgaag gaaggtgtgc gccttgatcg agtgcgtgga      540
332 ggccgtcaga aatacaagcg acggctggac tcagagagca gccatacct gagcttacia      600
334 atttctccac ctgctaataaa gccattgacc aagattgtct catacctact ggtggctgag      660
336 ccggacaagc tctatgccat gcctccccct ggtatgcctg agggggacat caaggccctg      720
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346 taccgggcca tcctgcagct ggtacgcagg tacaagaagc tcaagtgga gaaggaggag      1020
348 tttgtgacgc tcaaggccct ggccctcgcc aactccgatt ccatgtacat cgaggatcta      1080
350 gaggtgtcc agaagctgca ggacctgtg cacgaggcac tgcaggacta cgagctgagc      1140
352 cagcgccatg aggagccctg gaggacgggc aagctgctgc tgacactgcc gctgctgcgg      1200

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356 atgcacaaac tcttcctgga gatgctggag gccaaaggcct gggccagggc tgactccctt 1320
358 caggagtgga ggccactgga gcaagtgtccc tctcccctcc accgagccac caagaggcag 1380
360 catgtgcatt tcctaactcc cttgtcccct ccccatctg tggcctgggt gggcactgct 1440
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364 tag 1503
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368 <211> LENGTH: 436
369 <212> TYPE: PRT
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378 Lys Thr Glu Pro Ser Ser Pro Ala Ser Leu Thr Asp Ser Val Asn His
379 20 25 30
382 His Ser Pro Gly Gly Ser Ser Asp Ala Ser Gly Ser Tyr Ser Ser Thr
383 35 40 45
386 Met Asn Gly His Gln Asn Gly Leu Asp Ser Pro Pro Leu Tyr Pro Ser
387 50 55 60
390 Ala Pro Ile Leu Gly Gly Ser Gly Pro Val Arg Lys Leu Tyr Asp Asp
391 65 70 75 80
394 Cys Ser Ser Thr Ile Val Glu Asp Pro Gln Thr Lys Cys Glu Tyr Met
395 85 90 95
398 Leu Asn Ser Met Pro Lys Arg Leu Cys Leu Val Cys Gly Asp Ile Ala
399 100 105 110
402 Ser Gly Tyr His Tyr Gly Val Ala Ser Cys Glu Ala Cys Lys Ala Ser
403 115 120 125
406 Phe Lys Arg Lys Ile Gln Ala Asn Ile Glu Tyr Ser Cys Pro Ala Thr
407 130 135 140
410 Asn Glu Cys Glu Ile Thr Lys Arg Arg Arg Lys Ser Cys Gln Ala Cys
411 145 150 155 160
414 Arg Phe Met Lys Cys Leu Lys Val Gly Met Leu Lys Glu Gly Val Arg
415 165 170 175
418 Leu Asp Arg Val Arg Gly Gly Arg Gln Lys Tyr Lys Arg Arg Ile Asp
419 180 185 190
422 Ala Glu Asn Ser Pro Tyr Leu Asn Pro Gln Leu Val Gln Pro Ala Lys
423 195 200 205
426 Lys Pro Tyr Asn Lys Ile Val Ser His Leu Leu Val Ala Glu Pro Glu
427 210 215 220
430 Lys Ile Tyr Ala Met Pro Asp Pro Thr Val Pro Asp Ser Asp Ile Lys
431 225 230 235 240
434 Ala Leu Thr Thr Leu Cys Asp Cys Ala Asp Arg Glu Leu Val Val Ile
435 245 250 255
438 Ile Gly Trp Ala Lys His Ile Pro Gly Phe Ser Thr Leu Ser Leu Ala
439 260 265 270
442 Asp Gln Met Ser Leu Leu Gln Ser Ala Trp Met Glu Ile Leu Ile Leu
443 275 280 285
446 Gly Phe Val Tyr Arg Ser Leu Ser Phe Glu Asp Glu Leu Val Tyr Ala
447 290 295 300

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VERIFICATION SUMMARY

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